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Db 312 DIQAMEDSLQIQDSWATHNROFEESEBEFQTLKLLKPLSDRFLNSTALISQYWTMDSNLQHR 371
Qy 355 YEOLNSMKQLFLKAKQIVHKLFSLSKCHKOPILSPRTSTYMLTRIQSPLYCNG 414
Db 372 YQQLGASLKVLLKMKHRIVRRLFNLCRCHRPRLPKERSLSFWMNRISQSLYCGEST 431
Qy 415 LIGSFSETHSCTCPNDQVCTAFIPCTVGDASACLTICAPDNRTRCTGCTGTYMLSGGLC 474
Db 432 PGTFLEQSHSCTCPYDQSSCCGPIPCALGEGPACAHCSNDSTRCSGPNVGLAQLC 491
Qy 475 KPEVAESTDHYIGFETDLDLEKYLKQTDRIEVAHFIISNDMLNSWDFPSWKRML 534
Db 492 KPEVAESLEHFLGLEDLDLEKYLKQTDRIEVAHFIISNDMLNSWDFPSWKRML 551
Qy 535 LTLKSNKYKSLVHMLIGLSLQICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 594
Db 552 LTLKSNKYKPLVHVMALSLQICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 611
Qy 595 DWERTKLDLPQCYNTLTGNKWKTFETVHYILRSRIKSNPGNESIYYPELEFIDP 654
Db 612 DWERTNDVAAAQCNWITLGNRKTFETVHYILRSRIKSLDSSNETIYYPELEFIDP 671
Qy 655 SRNLGVMKINNIQVFGYSMHFDPPEAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 714
Db 672 SKNLGVMKINTLQVFGYSLPFPDAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 731
Qy 715 PGQRRLDLFSCLLRHRLKSTSEVVRISQALQAFNAKLNTWMDYDTTKLCS 766
Db 732 PGKVRDLDFSCLLRHRLKANNEVGRISQSLRAFNSKLPNPVEYETGKLCS 783

RESULT 5
Q80T96 PRELIMINARY; PRT; 788 AA.
ID Q80T96 AC Q80T96;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKTAA1747 protein (Fragment).
CN Name=6430517E21Rik; Synonyms=mKIAA1747;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=12693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA genes:
RT cDNAs identified by screening of terminal sequences of 400 mouse KIAA-homologous
RT randomly sampled from size-fractionated libraries.";
RL DNA Ref. 10:35-48(2003).
DR MGD; AKI22549; BAC65831.1;
DR MGD; MGI:2443333; 6430517E21Rik.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001862; MAC_perforin.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
FT NON_TER
SQ SEQUENCE 788 AA; 89748 MW; DF4189DAFD43705B CRC64;

Query Match 72.6%; Score 2963; DB 2; Length 788;
Best Local Similarity 70.7%; Ref. No. 9.2e-205;
Matches 546; Conservative 97; Mismatches 107; Indels 22; Gaps 5;

Qy 17 LW-----IALSLCHVLAFAA-----VSDQHATS-----PFDMLLSDKGPFHSQBY 60
Db 17 LWFPAFMAVLLALGVPGHVLAVSATVAAVVPEQVSSAGQAPLDLLTDRGFHQAQBY 76

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Qy 61 TDFVDSRQGFSTRYKIVREFGRMKNVNNLAVERNFLGSLPLAPEFRNIRLLGRPTL 130
Db 77 ADFMERYQGFSTRYKIVREFGRMKNVNNLALERRDFSLPLAPEFRNIRLLGRPTL 136
Qy 121 QQITENLKKYGTFFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTL 174
Db 137 QQVTENLKKYGTFFLLSATLGGESLTIFFVDRKLSKRAEGSDSTT-----NSSSVTL 196
Qy 175 ETLHOLAASVYDFDRSTRRLRHIIQIATAIKVTETGTPLGCSNYDNLDSVSVLQSP 234
Db 197 ETLHOLAASVYDFDRSTRRLRHIIQIATAIKVTETGTPLGCSNYDNLDSVSVLQSP 256
Qy 235 ENKIQQLQVLLPYLQERFVQAALSVIACNSGEFTCKENDCWCCHGCPKFPCEPCSM 294
Db 257 ENKVQLLQVLLPEHLRFRVAAALSYITCSSEGLVCHRENDCMCKSCPTTFECNCPDA 316
Qy 295 DIOAMENLRLITETWKAYNSDFEESDEFKLMRLPMNYFLANTSTIMHLMTWDSNFQRR 354
Db 317 DIOAMEDSLQIQDSWATHNROFEESEBEFQTLKLLKPLSDRFLNSTALISQYWTMDSNLQHR 376
Qy 355 YEOLNSMKQLFLKAKQIVHKLFSLSKCHKOPILSPRTSTYMLTRIQSPLYCNG 414
Db 372 YQQLGASLKVLLKMKHRIVRRLFNLCRCHRPRLPKERSLSFWMNRISQSLYCGEST 431
Qy 415 LIGSFSETHSCTCPNDQVCTAFIPCTVGDASACLTICAPDNRTRCTGCTGTYMLSGGLC 474
Db 432 PGTFLEQSHSCTCPYDQSSCCGPIPCALGEGPACAHCSNDSTRCSGPNVGLAQLC 496
Qy 475 KPEVAESTDHYIGFETDLDLEKYLKQTDRIEVAHFIISNDMLNSWDFPSWKRML 534
Db 492 KPEVAESLEHFLGLEDLDLEKYLKQTDRIEVAHFIISNDMLNSWDFPSWKRML 556
Qy 535 LTLKSNKYKSLVHMLIGLSLQICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 594
Db 552 LTLKSNKYKPLVHVMALSLQICLTQNSTLEPVLAVYVNPFGGSHSESFMFVNENFP 616
Qy 595 DWERTKLDLPQCYNTLTGNKWKTFETVHYILRSRIKSNPGNESIYYPELEFIDP 654
Db 612 DWERTNDVAAAQCNWITLGNRKTFETVHYILRSRIKSLDSSNETIYYPELEFIDP 676
Qy 655 SRNLGVMKINNIQVFGYSMHFDPPEAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 714
Db 672 SKNLGVMKINTLQVFGYSLPFPDAIRDLILQDYPYTGQSDSALLQLEIRDRVNKLS 736
Qy 715 PGQRRLDLFSCLLRHRLKSTSEVVRISQALQAFNAKLNTWMDYDTTKLCS 766
Db 732 PGKVRDLDFSCLLRHRLKANNEVGRISQSLRAFNSKLPNPVEYETGKLCS 788

RESULT 6
Q95560 PRELIMINARY; PRT; 781 AA.
ID Q95560 AC Q95560;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes S., (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-1999); CAA2893.1;
DR EMBL; AL032889; CAA2893.1;
DR InterPro; IPR006210; IEFG.
DR Pfam; PF01823; MACPF; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00457; MACPF; 1.
DR Hypothetical protein.
FT NON_TER

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SO SEQUENCE 781 AA; 88216 MW; DFE3EB83A088B599 CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 781;
 Best Local Similarity 70.6%; Pred. No. 1.1e-204;
 Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;

QY 16 ALMEW---IALSLHCWYLA---VSDQAT---SPFDWLLSDKGFPHRSOBYTDF 63
 DB 13 AVAPMTALLALGLPGWYLA---VSDQAT---SPFDWLLSDKGFPHRSOBYTDF 72

QY 64 VDRSQGFSTRYKRYEFGWKNVLAVERNPLGSPPLPAPEFNTLGLRRPTLOOI 123
 DB 73 MERYQGFSTRYKRYEFGWKNVLAVERNPLGSPPLPAPEFNTLGLRRPTLOOI 132

QY 124 TENLIKKGTHFLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 177
 DB 133 TENLIKKGTHFLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 192

QY 178 HOLAAASYFIDRSTLRRLHHIQTASTAIKVTETRTGPGCCSNYDNLDSVSVLVOSPENK 237
 DB 193 HOLAAASYFIDRSTLRRLHHIQTASTAIKVTETRTGPGCCSNYDNLDSVSVLVOSPENK 252

QY 238 IQLOGLVLLPDYLOERFVQAAALSYIACNSEGEFICKENDCWCCHGCPKPPCNCPSMDIQ 297
 DB 253 VOLGLQVLLPEYLRERFVQAAALSYIACNSEGEFICKENDCWCCHGCPKPPCNCPSMDIQ 312

QY 298 AMEENLRITETWKNYNSDFEESDEFKLMKRLPMNYFLNTSTIMHMTMDSNFORRYEQ 357
 DB 313 AMEENLRITETWKNYNSDFEESDEFKLMKRLPMNYFLNTSTIMHMTMDSNFORRYEQ 372

QY 358 LENSMLKOLFLKAAQIVHKLPSLRCHKOPLSLPRSTYMLTRIOSFLYCHENGLLG 417
 DB 373 LAGAKVLPKTHRLRLNLCRCRQPRFLPKRSLSTWNRIOSLCYGSESTPPG 432

QY 418 SFSETHSCTCPNDQVWCTAPLCTGDSACITCAPDNRTRCGTCNTGYMLSGCLCKPE 477
 DB 433 TFLQSHSCTCPYQSSCOQPIPCALGEGPACAHCAPDNRTRCGTCNTGYMLSGCLCKPE 492

QY 478 VAESTDHYIGPETDQLBNKYLKQTDRIEVAHPIPSNDRKLSNDFPWSRKMILLTL 537
 DB 493 VAESLENFLGLEDQLBNKYLKQTDRIEVAHPIPSNDRKLSNDFPWSRKMILLTL 552

QY 538 KENKYSLLVIMLGLSLOICLTKNSTLEPLVAVYVPPGSHSSSWPNVNSFPDWE 597
 DB 553 KENKYSLLVIMLGLSLOICLTKNSTLEPLVAVYVPPGSHSSSWPNVNSFPDWE 612

QY 598 RTKDLPLQCYNTLTLGNKWKTFETVHLYSRISKSPNGNSIYVEPLEFIDPSRN 657
 DB 613 RTNVDAAAOQNTLTLGNKWKTFETVHLYSRISKSPNGNSIYVEPLEFIDPSRN 672

QY 658 LGYKINNIQVGYSMHFDPEAIRDLILODYPTGOSDSSALLQILIRDRVNLSPRG 717
 DB 673 LGYKINNIQVGYSMHFDPEAIRDLILODYPTGOSDSSALLQILIRDRVNLSPRG 732

QY 718 QRRDLFSLRLHRLKLSSTSEVRISQALQAFNAKLPTMTDYDTTKLCS 766
 DB 733 KVRDLFSLRLHRLKLSSTSEVRISQALQAFNAKLPTMTDYDTTKLCS 781

RESULT 7

ID Q8N360 PRELIMINARY; PRT; 783 AA.

AC Q8N360; PRELIMINARY; PRT; 783 AA.

DT 01-OCT-2002 (TRENBLrel. 22, Created)

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DT 25-OCT-2004 (TRENBLrel. 22, Last annotation update)

DE BMP/retinoic acid-inducible neutral-specific protein 2 (DBCCR1-like2).

GN Name=KIAA1747; Synonyms=DBCCR1L2;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

SEQUENCE FROM N.A.

TISSUE=Brain;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stawston M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loeuvel N.A., Peters K.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., White M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Small U., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences";

RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE FROM N.A.

TISSUE=Brain;

RC Strausberg R.L.

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.

RA Inazawa J., Imoto I.;

RL "Homo sapiens DBCCR1.2 mRNA for DBCCR1-like2.";

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC028036; AAH28036.1; -

DR EMBL; AB161694; BAD34946.1; -

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001862; MAC_perforin.

DR Pfam; PF01823; MACPF; 1.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00457; MACPF; 1.

SEQUENCE 783 AA; 89004 MW; B8362095ADC97FCD CRC64;

Query Match 72.6%; Score 2962; DB 2; Length 783;
 Best Local Similarity 70.6%; Pred. No. 1.1e-204;
 Matches 543; Conservative 99; Mismatches 109; Indels 18; Gaps 4;

QY 16 ALMEW---IALSLHCWYLA---VSDQAT---SPFDWLLSDKGFPHRSOBYTDF 63
 DB 15 AVAPMTALLALGLPGWYLA---VSDQAT---SPFDWLLSDKGFPHRSOBYTDF 74

QY 64 VDRSQGFSTRYKRYEFGWKNVLAVERNPLGSPPLPAPEFNTLGLRRPTLOOI 123
 DB 75 MERYQGFSTRYKRYEFGWKNVLAVERNPLGSPPLPAPEFNTLGLRRPTLOOI 134

QY 124 TENLIKKGTHFLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 177
 DB 135 TENLIKKGTHFLSATLGGESLTFVDRKLSKRAEGSDSTT-----NSSSVTLETL 194

QY 178 HOLAAASYFIDRSTLRRLHHIQTASTAIKVTETRTGPGCCSNYDNLDSVSVLVOSPENK 237
 DB 195 HOLAAASYFIDRSTLRRLHHIQTASTAIKVTETRTGPGCCSNYDNLDSVSVLVOSPENK 254

QY 238 IQLOGLVLLPDYLOERFVQAAALSYIACNSEGEFICKENDCWCCHGCPKPPCNCPSMDIQ 297
 DB 255 VOLGLQVLLPEYLRERFVQAAALSYIACNSEGEFICKENDCWCCHGCPKPPCNCPSMDIQ 314

QY 298 AMEENLRITETWKNYNSDFEESDEFKLMKRLPMNYFLNTSTIMHMTMDSNFORRYEQ 357
 DB 315 AMEENLRITETWKNYNSDFEESDEFKLMKRLPMNYFLNTSTIMHMTMDSNFORRYEQ 374

QY 358 LENSMLKOLFLKAAQIVHKLPSLRCHKOPLSLPRSTYMLTRIOSFLYCHENGLLG 417
 DB 373 LAGAKVLPKTHRLRLNLCRCRQPRFLPKRSLSTWNRIOSLCYGSESTPPG 432

QY 418 SFSETHSCTCPNDQVWCTAPLCTGDSACITCAPDNRTRCGTCNTGYMLSGCLCKPE 477
 DB 433 TFLQSHSCTCPYQSSCOQPIPCALGEGPACAHCAPDNRTRCGTCNTGYMLSGCLCKPE 492

QY 478 VAESTDHYIGPETDQLBNKYLKQTDRIEVAHPIPSNDRKLSNDFPWSRKMILLTL 537
 DB 493 VAESLENFLGLEDQLBNKYLKQTDRIEVAHPIPSNDRKLSNDFPWSRKMILLTL 552

QY 538 KENKYSLLVIMLGLSLOICLTKNSTLEPLVAVYVPPGSHSSSWPNVNSFPDWE 597
 DB 553 KENKYSLLVIMLGLSLOICLTKNSTLEPLVAVYVPPGSHSSSWPNVNSFPDWE 612

QY 598 RTKDLPLQCYNTLTLGNKWKTFETVHLYSRISKSPNGNSIYVEPLEFIDPSRN 657
 DB 613 RTNVDAAAOQNTLTLGNKWKTFETVHLYSRISKSPNGNSIYVEPLEFIDPSRN 672

QY 658 LGYKINNIQVGYSMHFDPEAIRDLILODYPTGOSDSSALLQILIRDRVNLSPRG 717
 DB 673 LGYKINNIQVGYSMHFDPEAIRDLILODYPTGOSDSSALLQILIRDRVNLSPRG 732

QY 718 QRRDLFSLRLHRLKLSSTSEVRISQALQAFNAKLPTMTDYDTTKLCS 766
 DB 733 KVRDLFSLRLHRLKLSSTSEVRISQALQAFNAKLPTMTDYDTTKLCS 781